All TSS

Time Point 1

Time Point 2

Time Point 3

Time Point 4

Time Point 5

Time Point 6

Time Point 7

Time Point 8

Time Point 9

Time Point 10

Time Point 11

Time Point 12

Read Length (bp)

Distance from TSS (bp)
Ox Cluster TSS

Noceti_SupplementalFig 3
+1 Shift

Data from Yen et al.
### A. +1 Shift

- RNA

### B. RNA

- Ox

### C. Snf2

- snf2Δ/WT

### D. Srf2

- Peaks

### E. H3K9Ac

- Ox

### F. H3K14Ac

- Ox

### G. Gcn5

- Ox

### H. Dynamic Promoters

- Log2 Fold Change (snf2/WT)

- Activated

- Repressed
Supplemental Figure Legends

**Supplemental Figure 1 – Correlating +1 Shift to Transcriptional Activity for All Promoter Classes**

A. Normalized RNA RPKM values for each promoter through the YMC. R/B (Black), R/C (Blue), and Ox (Purple) clusters are marked to the right of the graph. Number of Taf1-Depleted (green), Taf1-Enriched (orange), and not assigned (grey) genes given along right side of heatmap.  
B. Normalized +1 shift associated with each promoter. Number of Taf1-Depleted (green), Taf1-Enriched (orange), and not assigned (grey) genes given along right side of heatmap.  
C. Number of Dynamic and Static promoters belonging to Ox, RB, RC, and NC clusters.  
D. Number of Dynamic and Static promoters belonging to TAF1 depleted and enriched categories.

**Supplemental Figure 2 – Uniform Digestion of Promoters Chromatin by MNase**

Heat-maps illustrating the average position of the upstream cut site made by MNase and ultimate read length for all promoters at each time-point.

**Supplemental Figure 3 – Uniform Digestion of Ox Phase Promoters Chromatin by MNase**

Heat-maps illustrating the average position of the upstream cut site made by MNase and ultimate read length for all Ox promoters at each time-point.

**Supplemental Figure 4 – RNA Abundance In The YMC vs Expression Pattern In Stationary Phase**
Stationary phase transcription data (Gasch et al. 2000) of ‘sentinel’ genes as defined by (Tu et al. 2005) plotted against raw RPKM transcript values through the YMC. Time points 1-6 shown in left column, and time points 7-12 are shown in right column.

**Supplemental Figure 5 - RNA Abundance In The YMC vs Expression Pattern in YPD**

Transcription data from yeast grown in rich media (Nagalakshmi et al. 2008) of ‘sentinel’ genes as defined by (Tu et al. 2005) plotted against raw RPKM values through the YMC. Time points 1-6 shown in left column, and time points 7-12 are shown in right column.

**Supplemental Figure 6 – Comparing Enrichment of Histone Modifications at Static and Dynamic Promoters**

Enrichment of H2AK5Ac, H2AS129Ph, H3K4Ac, H3K4me2, H3K4me3, H3K4me, H3K9Ac, H3K14Ac, H3K18Ac, H3K23Ac, H3K27Ac, H3K36me2, H3K36me3, H3K36me, H3K56Ac, H3K79me3, H3K79me, H3S10Ph, H4K5Ac, H4K8Ac, H4K12Ac, H4K16Ac, H4K20me, H4R3me2, H4R4me, Htz1 at Static (Black) and Dynamic (Blue) promoters. Data plotted against TSS.

**Supplemental Figure 7 – Enrichment of Chromatin Remodeling Factors According to +1 Shift**

Snf2, Rsc8, Isw2, Isw1, Ioc4, Ioc3, Ino80, and Arp5 binding at promoters organized by +1 shift (high to low from left to right). Dynamic and Static promoters are highlighted.

**Supplemental Figure 8 – Snf2, histone acetylation and Gcn5 are enriched at Ox genes.**

A, Normalized +1 Shift for each gene through 12 time points, data is separated into YMC super clusters according to RNA expression, Ox genes are highlighted in red box. B.
Gene Expression shown by normalized RPKM values from RNA-seq. C. Peaks of Snf2 binding within 100bp upstream and downstream of transcription start sites (Parnell et al. 2015). D. Change in transcript abundance as a result of snf2Δ in minimal media (Sudarsanam et al. 2000). E-G. Acetylation of H3K9 (E); H3K14 (F); and binding of Gcn5 (G) through the YMC (Kuang et al. 2014). Red triangles indicate Ox phase. H. Log2 expression fold change associated with Dynamic promoters belonging to each metabolic cluster in a snf2Δ background. Data from Sudarsanam et al. 2000.

**Supplemental Data 1**

File contains the chromosomal position and peak height of each nucleosome dyad annotated by iNPS for each of the twelve MNase digested samples analyzed.

**Supplemental Data 2**

This data file contains all raw transcript RPKM values associated with each gene for each of the twelve time points sampled.

**Supplemental Data 3**

This data file contains the positions and peak heights of +1 nucleosomes associated with each promoter for each of the twelve nucleosome libraries generated and analyzed in this study.